



1 CCCCTGGAC AGCCGCCCTC TCCCTCAGGC CCGTGGGGCT GGCCCTGCAC CGCCGAGCTT CCGGGGATGA GGGCCCCCGG TGTGTCACC CGGCGCGGCC
GGGGACCTG TCGGCGGGAG AGGAGGTCCG GGCACCCGGA CCGGGACGTG CGGGCTCGAA GGCCCTACT CCGGGGGGCC ACACCACTGG GCGCGCGCGG

101 CAGGTGCTG AGGAGCCCG GCCAGCGCG GAGATGGGG TGCACGTGA GTACTCGCG GCTGGCGCT CCGCCCGGCC CGGTCCCTG TTTGAGCGGG
GTCCAGGAC TCCCTGGGG CCGTCCCGC CTCTACCCC ACGTCCACT CATGACGCC CGACCCCGGA GGCGGGCGG GCGGAGGAC AAACCTCGGCC
1 M G V H
^Exon 1
^Met 1

201 GATTAGCG CGGGCTATT GGCCGGGAGG TGGTGGGT CAAGGACCG CGACTTGTA AGGACCCCG AGGGGGAGG GGGTGGGG AGCCTCCACG
CTAAATCGG GGCCGATAA CCGGCCCTCC ACCGACCAA GTTCTGGCC GCTGAACAGT TCCTGGGGCC TTCCCTCTCC CCCCACCCG TCGGAGGTGC

301 TGCCAGCGG GACTTGGGG AGTCTTGGG GATGGCAAAA ACCTGACCTG TGAAGGGGAC ACAGTTGGG GGTGAGGGG AAGAAGTTT GGGGTTCTG
ACGGTCGCC CTGAACCCCC TCAGGAACCC CTACCGTTT TGACTGGAC ACTTCCCTG TGCAAAACC CCAACTCCCC TTCTCCAAA CCCCCAAGC

401 CTGTGCCAST GGAGAGGAAG CTGATAAGCT GATAACCTGG GCGCTGAGC CACCACTTAT CTGCGAGAG GNNNTGGTA GCTGGGGTG GGGTGTGAC
GACACGTS A CTTCTCTTC GACTATTGA CTATTGACC CCGGACCTCG GTGGTAATA GACGCTCTCC CNNNNACCAT CGACCCCCAC CCGACACGTG

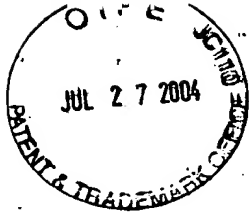
501 ACGGAGCAG GATTGAATGA AGGCAGGGA GGCAGCACCT GAGTGTTC ATGTTGGG ACAGGAAGGA CGAGCTGGG CAGAGACGTG GGGATGAAGG
TGCGTCGT CTAACCTACT TCCGTCCCT CCGTCCGTTA CTCAGGACG TACCAACCCC TGTCCTTCT GTCGACCCC GTCTCTGCAC CCCTACTTCC

601 AAGCTGTCT TCCACAGCCA CCCTTCTCCC TCCCGCCCTG ACTCTAGCC TGGTATCTC TTCTAGAAG TCTTGGCTGG CIGTGGCTIC ICCTGTCCCT
TTCGACAGGA AGGTGTCGT GGAAGAGGG AGGGCGGAC TGAGAGTCGG ACCGATAGG AAGATCTTAC AGGACGGACC GACACCGAAG AGGACAGGGA
1 E C P A W L W L L L S L
^Exon 2

701 GCTGTGCTC CCTCTGGGC TCCAGTCTT GGGGCCCCCA CCAGCCCTCA TCTGTGACG CCGAGTCTG GAGAGGTACC TCTGGAGGC CAAGGAGGCC
CGACAGGAG GGAGACCCGG AGGTACAGGA CCGCGGGGT GGTGGGAGT AGACACTGT GGTCTAGGAC CTCTCCATGG AGAACCCTCCG GTTCTCCCGG
13 L S L P L G L P V L G A P P R L I C D S R V L E R Y L L E A K E A

801 GAGATATCA CGGTGAGACC CCTTCCCCAG CACATTCCAC AGAATCAG CTCAGGGCTT CAGGGAATC CTCCAGATC CAGGAACCTG GCACTTGGT
CTCTTATAGT GCCACTCTGG GGAAGGGGTC GTGAAGGTG TCTTGAGTG GAGTCCGAA GTCCCTTGA GAGGGTCTAG GTCCTTGGAC CGTGAACCAA
46 E N I T

FIG. 1A



901	TGGGGTGGAG ACCCACCTC	TTGGGAAGCT AACCCCTTCGA	AGACACTGCC TCTGTGACGG	CCCTACATA GGGGATGTAT	AGATAAGTC TCTTATTGAG	TGGTGGCCCC ACCAACGGGG	AAACCATACC TTTGGTATGG	TGAAACTAG ACCTTTGATC	GCANGAGCA CGTTCCCGT	AAGCCAGCAG TTCGGTCGTC
1001	ATCCTAGGCG TAGGATGCCG	CTGTGGGCCA GACACCCGGT	GGGCCAGAGC CCCGGTCCTG	CTTCAGGAC GAAGTCCCTG	CCTTGACTCC GGAACGTGAGG	CCGGGCTGTG GGCCCGACAC	TGCATTTGAG ACGTAAAGTC	ACGGGCTGTG TGCCCGACAC	CCGAAACATG GGCTTGTGAC	CAGCTTGAAT GTGGAACCTA
1							T G C A ^ exon 3		E H C	S L N
1101	GAGAAATATCA CTCTTATAGT	CTGTCCCGAG GACAGGGTCT	CACCAAGTT GTGGTTTCAA	AATTTCATG TTAAAGATAC	CCTGGAAGAG GGACTTCTC	GATGAGGTG CTACCTCCAC	AGTTCCTTTT TCAAGGAA	TTTTTTTTT AAAAAANA	TCCTTTCTTT AGGAAAGAAA	TGAGAAATCT ACCTCTTAGA
11	E N I T	V P D	T K V	N F Y A	W K R	M E				
1201	CATTGGAG GTAAAGCTC	CCTGATTTG GGACTAANAAC	GATGAAGGG CTACTTTCCC	AGAATGATCG TCTTACTAGC	AGGGAAGGT TCCCTTTCCA	AAATGGAGC TTTTACTCTG	AGCAGAGATG TCGTCTCTAC	AGGTGCTCTG TCCGACGGAC	GGCGCAGAGG CCGCGTCTCC	CTCACGTCTA GAGTGCAGAT
1301	TAATCCAGG ATTAGGGTCC	CTGAGATGGC GACTCTACCG	CGAGATGGGA GCTCTACCCCT	GAATTGCTTG CTTAAGGAAC	AGCCCTGGAG TCGGGACCTC	TTTCAGACCA AAAGTCTGGT	ACCTGGGAG TGGAACCGTC	CATAGTGAGA GTATCACTCT	TCCCCCATCT AGGGGGTAGA	CTACAAACAT GATGTTTGTG
1401	TTAAANAAT AATTTTTTAA	TAGTCAGGTG ATCAGTCCAC	AGGTGGTGCA TCCACCAGGT	TGGTGGTAGT ACCACCATCA	CCCAGATATT GGGTCTATAA	TGGAAGGCTG ACCTTCCGAC	AGGCGGGAGG TCCGCCCTCC	ATCGCTTGAG TAGCGAACTC	CCCAGGAATT GGTCTCTTAA	TGAGGCTGCA ACTCCGAGCT
1501	GTGAGCTGTG CACTCGACAC	ATCACACCAC TAGTGTGGTG	TGCATCCGAG ACGTGAGGTC	CCTCAGTGAC GGAGTCACTG	AGAGTGAGGC TCTCACTCCG	CCTGTCTCAA GGACAGAGTT	AAAAGAAAG TTTTCTTTC	AAAAAAGAAA TTTTTTTTT	AATAATGAGG TTATTACTCC	GCTGTATGGA GCACATACCT
1601	ATACATTCAT TATGTAAAGTA	TATTCATTCA ATAAGTAAAGT	CTCACTCATT GAGTGAGTAA	CATTCAATCA GTAAGTAAAGT	TTCAATTCNN AAGTAAAGNN	NNNTCTTATT NNNAGATATA	GCATACCTCT CGTATGGAGA	GTTTGTCTCAG CAAAGAGTC	CTTGGTGTCT GAACCAAGAA	GGGGCTGTG CCCCGACGAC
1701	AGGGCAGGA TCCCCGTCTCT	GGGAGAGGT CCCTCTCCCA	GGCATGGGTC CCGTACCCAG	AGCTGACTCC TCGACTGAGG	CAGAGTCCAC GTCTCAGGTG	TCCTGTAGG AGGGACATCC	TCAGGCGAGCA AGTCCGTGCT	GGCCGTAGAA CCGGCATCTT	GTCTGGCAGG CAGACCCGTCC	GCCTGGCCCT CGGACCCGGA
1						V ^	R Q Q	A V E	V W Q G	L A L
1801	GCTCTCGGAA CGAGAGCCTT	GCTGTCTGCT CGACAGGACG	GGGCCAGGC CCCCGTCCG	CCTGTGCTC GGACAAACAG	AACCTTCCC TTGAGAGGG	AGCCGTGGGA TGGCACCTT	GCCCTGCGAG CGGGGACGTC	CTGCATGTGG GACGTACACC	ATAAGCCGT TATTTCCGCA	CAGTGGCCTT GTCACCCGAA
15	L S E	A V L R	G Q A	L L V	N S S Q	P W E	P L Q	L H V D	K A V	S G L
1901	CGAGCCTCA GGTCCGAGT	CCACTCTGCT GGTGAGACGA	TCGGGCTCTG AGCCCGAGAC	GGAGCCCGAG CCTCGGTCC	TGAGTAGGAG ACTCATCTCT	CGACACTTC GCTGTGAGG	TGCTTCCCT ACGAACGGGA	TTCTGTGAAGA AAGACATCT	AAGGGAGAAG TTCCCTCTTC	GGTCTTGTCTA CCAGAACGAT
48	B S I T	T L L	B A L	G A O						

FIG. 1B



2001 AGGAGTACAG GAACGTGICCG TATTCCTTCC CCTTCTGTGG CACTGCAGCG ACCTCCTGTT TTCTCCTTGG CAGAAGGAAG CCATCTCCCC TCCAGATGCG
TCCTCATGTC CTTGACAGGC ATAAGGAAGG GGAAGACACC GTGACGTGCG TGGAGGACAA AAGAGGAACC GTCTTCTTTC GGTAGAGGGG AGGTCTACCG
1 K E A I S P P D A
^exon 5
2101 GCCTCAGCTG CTCCACTCCG AACAATCACT GCTGACACTT TCCGCAACT CTTCGAGTC TACICCAATT TCCTCCGGGG AAAGCTGAAG CTGTACACAG
CGGAGTCGAG GAGGTGAGGC TTGTTAGTGA CGACTGTGAA AGCGTTTGA GAAGGCTCAG ATGAGGTAA AGGAGGCCCG TTTCGACTTC GACATGTGTC
10 A S A A P L R T I T A D T F R K L F R V Y S N F L R G K L K L Y T G
2201 GGGAGGCC TG CAGGACAGGG GACAGATGAC CAGGTGTGTC CACTGGGCA TATCCACCAC CTCCCTCACC AACATTGCTT GTGCCACACC CTCCCCCGCC
CCCTCCGGAC GTCCGTGTCCT CTGTCTACTG GTCCACACAG GTGGACCCGT ATAGGTGGTG GAGGGAGTGG TTGTAACGAA CACGGTGTGG GAGGGGGGGG
44 E A C R T G D R O
2301 ACTCCTGAAC CCCGTCGAGG AGCTCTCAG
TGAGGACTTG GGGCAGCTCC TCGAGAGTC

FIG. 1C



1	ATGGGGTGC	ACGAATGTC	TGCCTGGCTG	TGGCTTCTCC	TGTCCTTGCT	GTGCTCCCT	CTGGGCTCC	CAGTCTGGG	CGCCCCACCA	GCCCTCATCT
1	TACCCCAAG	TGCTTACAG	ACGGACCGAC	ACCGAAGAG	ACAGGACGA	CAGCGAGGA	GACCGGAGG	GTCAGGACC	GCGGGGTGGT	GCGGAGTAG
	M G V H	E C P	A W L	W L L L	S L L	S L P	L G L P	V L G	A P P	R L I C
101	GTGACAGCG	AGTCTGGAG	AGGTACTCT	TGGAGGCCAA	GGAGGCCGAG	AATATCACGA	CGGCTGTGC	CGAACACTGC	AGCTTGAATG	AGAATATCAC
35	CACTGTGCG	TCAGGACCTC	TCCATGGAGA	ACCTCCGTT	CCTCCGCTC	TTATAGTGT	GCCGACACG	GCTTGTGACG	TCGAACCTTAC	TCTTATAGTG
	D S R	V L E	R Y L L	E A K	E A E	N I T T	G C A	E H C	S L N E	N I T
										*
201	TGTCCAGAC	ACCAAAGTTA	ATTCTATGC	CTGGAAGAG	ATGGAGTCA	GGCAGCAGG	CGTAGAAGTC	TGGCAGGGCC	TGGCCCTGCT	CTCGGAAGCT
68	ACAGGGTCTG	TGGTTTCAAT	TAAAGATACG	GACCTTCTCC	TACCTCCAGT	CCGTGCTCCG	GCATCTTCAG	ACCGTCCCG	ACCGGACGA	GAGCCTTCGA
	V P D	T K V N	F Y A	W K R	M E V R	Q Q A	V E V	W Q G L	A L L	S E A
301	GTCCTGCGG	GCCAGGCCCT	GTTGTCAC	TCTTCCAGC	CGTGGAGCC	CCTGCAGCTG	CATGTGGATA	AAGCCGTACG	TGGCCTTCGC	AGCCTCACCA
101	CAGGACGCC	CGGTCCGGA	CAACCACTTG	AGAGGGTCG	GCACCTCGG	GGACCTCGAC	GTACACCTAT	TTCGGCAGTC	ACCGGAAGCG	TCGGAGTGGT
	V L R G	Q A L	L V N	S S Q P	W E P	L Q L	H V D K	A V S	G L R	S L T T
401	CTCTGCTTCG	GGCTCTGGGA	GCCCAGAAGG	AAGCCATCTC	CCCTCCAGAT	GCGGCTCAG	CTGCTCCACT	CCGAACAATC	ACTGCTGACA	CTTTCGCAA
135	GAGACGAGC	CCGAGACCTT	CGGTCTTCC	TTCGGTAGAG	GGGAGTCTA	CGCCGAGTC	GACGAGGTGA	GGCTTGTAG	TGACGACTGT	GAAAGGCGTT
	L L R	A L G	A Q K E	A I S	P P D	A A S A	A P L	R T I	T A D T	F R K
501	ACTCTTCCGA	GTCTACTCCA	ATTTCTCTCG	GGGAAAGCTG	AAGCTGTACA	CAGGGAGGC	CTGCAGGACA	GGGACAGAT	GACCA	
148	TGAGAAGGCT	CAGATGAGGT	TAAAGGAGGC	CCCTTTCGAC	TTGACATGT	GTCCCTCCG	GACCTCCTGT	CCCCTGTCTA	CTGGT	
	L F R	V Y S N	F L R	G K L	K L Y T	G E A	C R T	G D R O		

FIG.2



HUMAN	MGVHECPAWLWLLSLLSLPLGLPVLGAPPRLLCDSRVLYLLEAKEAE *****
CHEPO	MGVHECPAWLWLLSLLSLPLGLPVLGAPPRLLCDSRVLYLLEAKEAE *****
HUMAN	NITGCAEHCSLNENITVPTKVNFYAWKRMEVGQQAQVEVWQLALLSEA *****
CHEPO	NITGCAEHCSLNENITVPTKVNFYAWKRMEVGQQAQVEVWQLALLSEA *****
HUMAN	VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD *****
CHEPO	VLRGQALLVNSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAISPPD *****
HUMAN	AASAAPLRITITADTFRKLFVYSNFLRGKCLKLYTGEACRTGDR *****
CHEPO	AASAAPLRITITADTFRKLFVYSNFLRGKCLKLYTGEACRTGDR *****

FIG.3



Application No.: 09/813,775
Filing Date: March 20, 2001
Title: Novel Chimpanzee Erythropoietin
(CHEPO) Polypeptides...
Docket No.: 39755-0057 CP2
Sheet 6 of 7

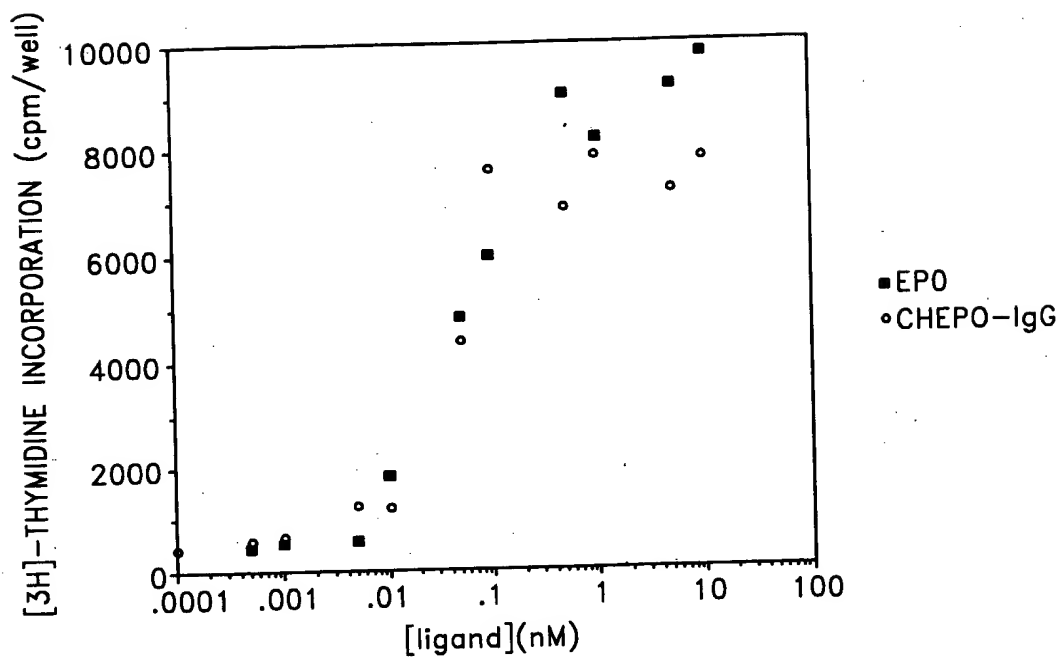


FIG. 4

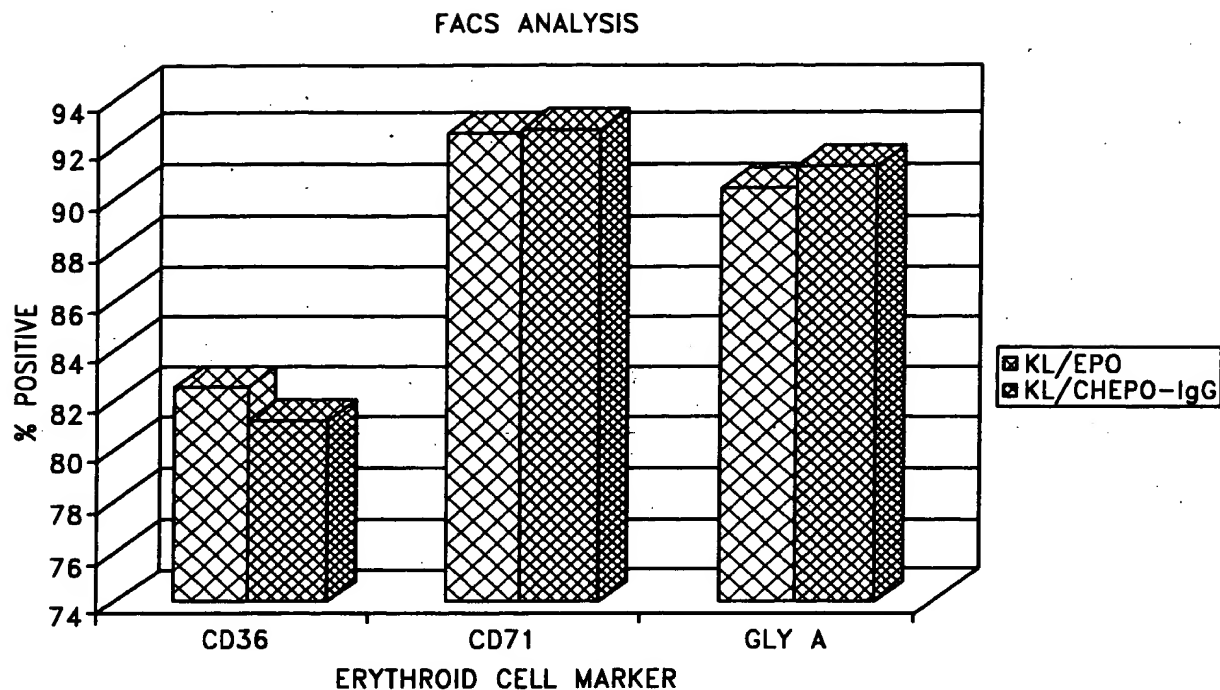


FIG.5